

Gambel

#5

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/013,871A

DATE: 02/12/1999
TIME: 08:40:34

INPUT SET: S30613.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANTS: MARTIN, Ulrich; HASSELBECK, Anton; SCHUMACHER, Guenther;
CO, Man S.

(ii) TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF
MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR
PREVENTION OF ACUTE ORGAN DAMAGE AFTER
EXTRACORPOREAL BLOOD CIRCULATION

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Felfe & Lynch
(B) STREET: 805 Third Avenue
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: U.S.A.
(F) ZIP: 10022

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" Computer Disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: ASCII, WordPerfect 5.1

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/013,871
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/578,953
(B) FILING DATE: 27-Dec-95

(A) APPLICATION NUMBER: EP 95 112 895.8
(B) FILING DATE: 17-Aug-95

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: EP 95 114 969.9
(B) FILING DATE: 19-Sep-95

(viii) ATTORNEY/AGENT INFORMATION

(A) NAME: Hanson, Norman D.

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47      (B) REGISTRATION NUMBER: 30,946
48      (C) REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH
49
50      (ix) TELECOMMUNICATION INFORMATION
51          (A) TELEPHONE: (212) 688-9200
52          (B) TELEFAX: (212) 838-3884
53      (2) INFORMATION FOR SEQ ID NO: 1:
54
55          (i) SEQUENCE CHARACTERISTICS:
56              (A) LENGTH: 654 base pairs
57              (B) TYPE: nucleic acid
58              (C) STRANDEDNESS: double
59              (D) TOPOLOGY: linear
60
61          (ii) MOLECULE TYPE: cDNA
62
63          (ix) FEATURE:
64              (A) NAME/KEY: CDS
65              (B) LOCATION: 1,,654
66
67          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
68
69      GAC ATT CAG ATG ACC CAA TCT CCG AGC TCT TTG TCT GCG TCT GTA GGG 48
70      Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
71      1 5 10 15
72
73      GAT AGG GTC ACT ATC ACC TGC AAG GCC AGC CAA AGT GTT GAT TAT GAT 96
74      Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
75      20 25 30
76
77      GGT GAT AGT TAT ATG AAC TGG TAC CAA CAG AAA CCA GGA AAG GCA CCC 144
78      Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
79      35 40 45
80
81      AAG CTT CTC ATC TAT GCT GCA TCC AAC CTA GAA TCT GGT ATC CCA TCC 192
82      Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ser
83      50 55 60
84
85      AGG TTT AGT GGC AGT GGG TCT GGG ACA GAC TTC ACC CTC ACC ATC TCT 240
86      Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
87      65 70 75 80
88
89      TCT CTG CAG CCG GAG GAT TTC GCA ACC TAT TAC TGT CAG CAA AGT AAT 288
90      Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn
91      85 90 95
92
93      GAA GAT CCG TGG ACG TTC GGT CAA GGC ACC AAG GTG GAA ATC AAA CGA 336
94      Glu Asp Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
95      100 105 110
96
97      ACT GTG GCT GCA CCA TCT GTC TTC ATC TTC CCG CCA TCT GAT GAG CAG 384
98      Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
99      115 120 125

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100
101 TTG AAA TCT GGA ACT GCC TCT GTT GTG TGC CTG CTG AAT AAC TTC TAT 432
102 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
103 130 135 140
104
105 CCC AGA GAG GCC AAA GTA CAG TGG AAG GTG GAT AAC GCC CTC CAA TCG 480
106 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
107 145 150 155 160
108
109 GGT AAC TCC CAG GAG AGT GTC ACA GAG CAG GAC AGC AAG GAC AGC ACC 528
110 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
111 165 170 175
112
113 TAC AGC CTC AGC AGC ACC CTG ACG CTG AGC AAA GCA GAC TAC GAG AAA 576
114 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
115 180 185 190
116
117 CAC AAA GTC TAC GCC TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG CCC 624
118 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
119 195 200 205
120
121 GTC ACA AAG AGC TTC AAC AGG GGA GAG TGT 654
122 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
123 210 215
124
125
126
127 (2) INFORMATION FOR SEQ ID NO: 2:
128
129 (i) SEQUENCE CHARACTERISTICS:
130 (A) LENGTH: 218
131 (B) TYPE: amino acid
132 (C) STRANDEDNESS: single
133 (D) TOPOLOGY: linear
134
135 (ii) MOLECULE TYPE: protein
136
137 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
138
139 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
140 1 5 10 15
141
142 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
143 20 25 30
144
145 Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
146 35 40 45
147
148 Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ser
149 50 55 60
150
151 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
152 65 70 75 80

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153
154 Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn
155                      85                      90                      95
156
157 Glu Asp Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
158                100                105                110
159
160 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
161                115                120                125
162
163 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
164                130                135                140
165
166 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
167 145                150                155                160
168
169 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
170                165                170                175
171
172 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
173                180                185                190
174
175 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
176                195                200                205
177
178 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
179 210                215
180
181
182
183 (2) INFORMATION FOR SEQ ID NO: 3:
184
185 (i) SEQUENCE CHARACTERISTICS:
186 (A) LENGTH: 1329 base pairs
187 (B) TYPE: nucleic acid
188 (C) STRANDEDNESS: double
189 (D) TOPOLOGY: linear
190
191 (ii) MOLECULE TYPE: cDNA
192
193 (ix) FEATURE:
194 (A) NAME/KEY: CDS
195 (B) LOCATION:1,,1329
196
197 (ix) FEATURE:
198 (A) NAME/KEY: mat_peptide
199 (B) LOCATION:1
200
201 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
202
203 GAA GTG CAA CTG GTG GAG TCT GGG GGA GGC TTA GTG CAG CCT GGA GGA 48
204 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
205 1 5 10 15

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206
207 AGC TTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACT TTC AGT ACC TAT 96
208 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
209                20                25                30
210
211 GCC ATG TCT TGG GTT CGC CAG GCT CCA GGG AAG GGA CTC GAG TGG GTC 144
212 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
213                35                40                45
214
215 GCA TCC ATT AGT ACT GGT GGT AGC ACC TAC TAT CCA GAC AGT GTG AAG 192
216 Ala Ser Ile Ser Thr Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val Lys
217                50                55                60
218
219 GGC CGA TTC ACC ATC TCC AGA GAT AAT GCC AAG AAC ACC CTG TAC CTG 240
220 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu
221        65                70                75                80
222
223 CAA ATG AAT TCT CTG AGG GCT GAG GAC ACG GCC GTG TAT TAC TGT GCA 288
224 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
225                85                90                95
226
227 AGA GAC TAT GAC GGG TAT TTT GAC TAC TGG GGC CAA GGC ACC CTG GTC 336
228 Arg Asp Tyr Asp Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
229                100                105                110
230
231 ACA GTC TCC TCA GCT TCC ACC AAG GGC CCA TCC GTC TTC CCC CTG GCG 384
232 Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
233                115                120                125
234
235 CCC TGC TCC AGG AGC ACC TCC GAG AGC ACA GCC GCC CTG GGC TGC CTG 432
236 Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
237                130                135                140
238
239 GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC 480
240 Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
241        145                150                155                160
242
243 GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA 528
244 Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
245                165                170                175
246
247 GGA CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG 576
248 Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
249                180                185                190
250
25

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